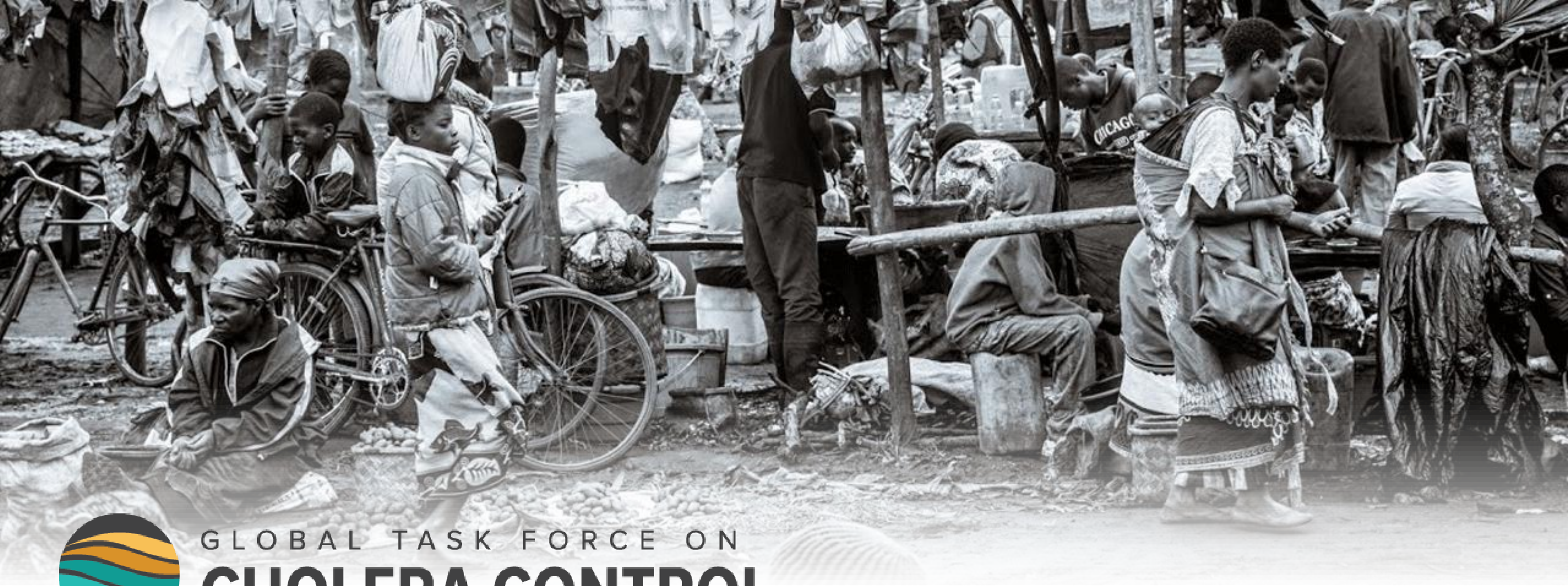

GLOBAL TASK FORCE ON CHOLERA CONTROL

GTFCC LABORATORY WORKING GROUP: GTFCC TECHNICAL NOTE ON DNA BASED IDENTIFICATION

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BACKGROUND

CURRENT PUBLISHED TECHNICAL NOTE

- Title: **Interim Technical Note Introduction of DNA-based identification and typing methods to public health practitioners for epidemiological investigation of cholera outbreaks.**
- Objective: **To provide information summarizing the added value of monitoring of toxigenic *Vibrio cholerae* strains using DNA-based techniques as part of comprehensive cholera prevention and control.**
- Date published: June 2017
- Urgent need to update!

BENEFITS OF SARS-COV2 PANDEMIC

- **PCR:**
  - Found in almost every country!
  - Became routine methodology almost globally.
- **NGS:**
  - Becoming more and more affordable
  - Accessible in the majority of countries
  - Hubs for sequencing established

SHOULDN'T WE BENEFIT FROM THE EXISTING PLATFORMS?

WAY FORWARD

SURVEILLANCE GUIDELINES-2024

- Not for diagnostic purposes; for further characterisation of a strain
- WGS does not aim to confirm *Vibrio cholerae* as the causative agent in an outbreak, but can confirm that strains belong to the seventh pandemic El Tor lineage (7PET) or any lineage that might emerge with similar clinical and epidemiological properties
- WGS, as well as other advanced genotyping methods, can provide important additional information which be used to establish a relationship between ongoing and previous outbreaks, track the genetic evolution of Vibrio cholerae strains, detect the emergence of new clones, and conduct phylogenetic analyses to enable the visualisation of the worldwide circulation and evolution of strains.

KEY POINTS TO CONSIDER

- Focus on publishing new recommendations with regards to sequencing
- Work on a separate technical note for PCR
- Highlight and focus on when is sequencing useful!
- Discuss the frequency of using NGS in an outbreak setting and the number of samples to sequence
- Discuss available platforms for sequencing
- Stress on the importance of data sharing
- Highlight the type of information that can be retrieved from sequencing.

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THANK YOU